



# REPLACEMENT FIGURE

Figure 2

CATGGAGC	CCGAGTGAGC	GCGGCGCGGG	CCCGTCCGGC	CGCCGGACAA	CATGGAGGCA	60
GCGCCGCCCG	GGCCGCCCGT	GCCGCTGCTG	CTGCTGCTGC	TGCTGCTGCT	GGCGCTGTGC	120
GGCTGCCCGG	CCCCGCCCGC	GGCCTCGCCG	CTCCTGCTAT	TTGCCAACCG	CCGGGACGTA	180
CGGCTGGTGG	ACGCCGGCGG	AGTCAAGCTG	GAGTCCACCA	TCGTGGTCAG	CGGCCTGGAG	240
GATGCGGCCG	CAGTGGACTT	CCAGTTTTTC	AAGGGAGCCG	TGTACTGGAC	AGACGTGAGC	300
GAGGAGGCCA	TCAAGCAGAC	CTACCTGAAC	CAGACGGGGG	CCGCCGTGCA	GAACGTGGTC	360
ATCTCCGGCC	TGGTCTCTCC	CGACGGCCTC	GCCTGCGACT	GGGTGGGCAA	GAAGCTGTAC	420
TGGACGGACT	CAGAGACCAA	CCGCATCGAG	GTGGCCAACC	TCAATGGCAC	ATCCCGGAAG	480
GTGCTCTTCT	GGCAGGACCT	TGACCAGCCT	AGGGCCATCG	CCTTGGACCC	CGCTCACGGG	540
TACATGTACT	GGACAGACTG	GGGTGAGACG	CCCCGGATTG	AGCGGGCAGG	GATGGATGGC	600
AGCACCCGGA	AGATCATTGT	GGACTCGGAC	ATTTACTGGC	CCAATGGACT	GACCATCGAC	660
CTGGAGGAGC	AGAAGCTCTA	CTGGGCTGAC	GCCAAGCTCA	GCTTCATCCA	CCGTGCCAAC	720
CTGGACGGCT	CGTTCCGGCA	GAAGGTGGTG	GAGGGCAGCC	TGACGCACCC	CTTCGCCCTG	780
ACGCTCTCCG	GGGACACTCT	GTACTGGACA	GACTGGCAGA	CCCGCTCCAT	CCATGCCTGC	840
AACAAGCGCA	CTGGGGGGAA	GAGGAAGGAG	ATCCTGAGTG	CCCTCTACTC	ACCCATGGAC	900
ATCCAGGTGC	TGAGCCAGGA	GCGGCAGCCT	TTCTTCCACA	CTCGCTGTGA	GGAGGACAAT	960
GGCGGCTGCT	CCCACCTGTG	CCTGCTGTCC	CCAAGCGAGC	CTTTCTACAC	ATGCGCCTGC	1020
CCCACGGGTG	TGCAGCTGCA	GGACAACGGC	AGGACGTGTA	AGGCAGGAGC	CGAGGAGGTG	1080
CTGCTGCTGG	CCCGGCGGAC	GGACCTACGG	AGGATCTCGC	TGGACACGCC	GGACTTCACC	1140
GACATCGTGC	TGCAGGTGGA	CGACATCCGG	CACGCCATTG	CCATCGACTA	CGACCCGCTA	1200
GAGGGCTATG	TCTACTGGAC	AGATGACGAG	GTGCGGGCCA	TCCGCAGGGC	GTACCTGGAC	1260
GGGTCTGGGG	CGCAGACGCT	GGTCAACACC	GAGATCAACG	ACCCCGATGG	CATCGCGGTC	1320
GACTGGGTGG	CCCGAAACCT	CTACTGGACC	GACACGGGCA	CGGACCGCAT	CGAGGTGACG	1380
CGCCTCAACG	GCACCTCCCG	CAAGATCCTG	GTGTGCGGAG	ACCTGGACGA	GCCCCGAGCC	1440
ATCGCACTGC	AGCCCGTGAT	GGGCCTCATG	TACTGGACAG	ACTGGGGAGA	GAACCCTAAA	1500
ATCGAGTGTG	CCAACCTGGA	TGGGCAGGAG	CGGCGTGTGC	TGGTCAATGC	CTCCCTCGGG	1560
TGGCCCAACG	GCCTGGCCCT	GGACCTGCAG	GAGGGGAAGC	TCTACTGGGG	AGACGCCAAG	1620
ACAGACAAGA	TCGAGGTGAT	CAATGTTGAT	GGGACGAAGA	GGCGGACCCT	CCTGGAGGAC	1680
AAGCTCCCGC	ACATTTTCGG	GTTACAGCTG	CTGGGGGACT	TCATCTACTG	GACTGACTGG	1740
CAGCGCCGCA	GCATCGAGCG	GGTGACAAG	GTCAAGGCCA	GCCGGGACGT	CATCATTGAC	1800
CAGCTGCCCC	ACCTGATGGG	GCTCAAAGCT	GTGAATGTGG	CCAAGGTCGT	CGGAACCAAC	1860
CCGTGTGCGG	ACAGGAACGG	GGGGTGACG	CACCTGTGCT	TCTTCACACC	CCACGCAACC	1920
CGGTGTGGCT	GCCCCATCGG	CCTGGAGCTG	CTGAGTGACA	TGAAGACCTG	CATCGTGCCT	1980
GAGGCCTTCT	TGGTCTTCAC	CAGCAGAGCC	GCCATCCACA	GGATCTCCCT	CGAGACCAAT	2040
AACAACGACG	TGGCCATCCC	GCTCACGGGC	GTCAAGGAGG	CCTCAGCCCT	GGACTTTGAT	2100
GTGTCCAACA	ACCACATCTA	CTGGACAGAC	GTCAGCCTGA	AGACCATCAG	CCGCGCCTTC	2160
ATGAACGGGA	GCTCGGTGGA	GCACGTGGTG	GAGTTTGGCC	TTGACTACCC	CGAGGGCATG	2220
GCCGTTGACT	GGATGGGCAA	GAACCTCTAC	TGGGCCGACA	CTGGGACCAA	CAGAATCGAA	2280
GTGGCGCGGC	TGGACGGGCA	GTTCCGGCAA	GTCTCTGTGT	GGAGGGACTT	GGACAACCCG	2340
AGGTCGCTGG	CCCTGGATCC	CACCAAGGGC	TACATCTACT	GGACCGAGTG	GGGCGGCAAG	2400
CCGAGGATCG	TGCGGGCCTT	CATGGACGGG	ACCAACTGCA	TGACGCTGGT	GGACAAGGTG	2460
GGCCGGGCCA	ACGACCTCAC	CATTGACTAC	GCTGACCAGC	GCCTCTACTG	GACCGACTG	2520
GACACCAACA	TGATCGAGTC	GTCCAACATG	CTGGGTGAGG	AGCGGGTCGT	GATTGCCGAC	2580
GATCTCCCGC	ACCCGTTCCG	TCTGACGCAG	TACAGCGATT	ATATCTACTG	GACAGACTGG	2640
AATCTGCACA	GCATTGAGCG	GGCCGACAAG	ACTAGCGGCC	GGAACCGCAC	CCTCATCCAG	2700
GGCCACCTGG	ACTTCGTGAT	GGACATCCTG	GTGTTCCACT	CCTCCCGCCA	GGATGGCCTC	2760
AATGACTGTA	TGCACAACAA	CGGGCAGTGT	GGGCAGCTGT	GCCTTGCCAT	CCCCGGCGGC	2820
CACCGCTGCG	GCTGCGCCTC	ACACTACACC	CTGGACCCCA	GCAGCCGCAA	CTGCAGCCCG	2880
CCCACCACCT	TCTTGCTGTT	CAGCCAGAAA	TCTGCCATCA	GTCGGATGAT	CCCGGACGAC	2940
CAGCACAGCC	CGGATCTCAT	CCTGCCCCCTG	CATGGACTGA	GGAACGTCAA	AGCCATCGAC	3000
TATGACCCAC	TGGACAAGTT	CATCTACTGG	GTGGATGGGC	GCCAGAACAT	CAAGCGAGCC	3060
AAGGACGACG	GGACCCAGCC	CTTTGTTTTG	ACCTCTCTGA	GCCAAGGCCA	AAACCCAGAC	3120
AGGCAGCCCC	ACGACCTCAG	CATCGACATC	TACAGCCGGA	CACTGTTCTG	GACGTGCGAG	3180
GCCACCAATA	CCATCAACGT	CCACAGGCTG	AGCGGGGAAG	CCATGGGGGT	GGTGTGCGT	3240

## REPLACEMENT FIGURE

Figure 2

GGGGACCGCG	ACAAGCCCAG	GGCCATCGTC	GTCAACGCGG	AGCGAGGGTA	CCTGTACTTC	3300
ACCAACATGC	AGGACCGGGC	AGCCAAGATC	GAACGCGCAG	CCCTGGACGG	CACCGAGCGC	3360
GAGGTCCTCT	TCACCACCGG	CCTCATCCGC	CCTGTGGCCC	TGGTGGTGGA	CAACACACTG	3420
GGCAAGCTGT	TCTGGGTGGA	CGCGGACCTG	AAGCGCATTG	AGAGCTGTGA	CCTGTCAGGG	3480
GCCAACCGCC	TGACCCTGGA	GGACGCCAAC	ATCGTGCAGC	CTCTGGGCCT	GACCATCCTT	3540
GGCAAGCATC	TCTACTGGAT	CGACCGCCAG	CAGCAGATGA	TCGAGCGTGT	GGAGAAGACC	3600
ACCGGGGACA	AGCGGACTCG	CATCCAGGGC	CGTGTGCCCC	ACCTCACTGG	CATCCATGCA	3660
GTGGAGGAAG	TCAGCCTGGA	GGAGTTCTCA	GCCCCACCAT	GTGCCCCGTA	CAATGGTGGC	3720
TGCTCCCACA	TCTGTATTGC	CAAGGGTGAT	GGGACACCAC	GGTGCTCATG	CCCAGTCCAC	3780
CTCGTGCTCC	TGCAGAACCT	GCTGACCTGT	GGAGAGCCGC	CCACCTGCTC	CCCGGACCAG	3840
TTTGATGTG	CCACAGGGGA	GATCGACTGT	ATCCCCGGGG	CCTGGCGCTG	TGACGGCTTT	3900
CCCGAGTGCG	ATGACCAGAG	CGACGAGGAG	GGCTGCCCCG	TGTGCTCCGC	CGCCCAGTTC	3960
CCCTGCGCGC	GGGGTCAGTG	TGTGGACCTG	CGCCTGCGCT	GCGACGGCGA	GGCAGACTGT	4020
CAGGACCGCT	CAGACGAGGC	GGACTGTGAC	GCCATCTGCC	TGCCCCAACCA	GTTCGGGTGT	4080
GCGAGCGGCC	AGTGTGTCTT	CATCAAACAG	CAGTGCGACT	CCTTCCCCGA	CTGTATCGAC	4140
GGCTCCGACG	AGCTCATGTG	TGAAATCACC	AAGCCGCCCT	CAGACGACAG	CCCGGCCAC	4200
AGCAGTGCCA	TCGGGCCCCG	CATTGGCATC	ATCCTCTCTC	TCTTCGTCAT	GGGTGGTGTC	4260
TATTTTGTGT	GCCAGCGCGT	GGTGTGCCAG	CGCTATGCGG	GGGCCAACGG	GCCCTTCCCG	4320
CACGAGTATG	TCAGCGGGAC	CCCGCACGTG	CCCCTCAATT	TCATAGCCCC	GGGCGGTTC	4380
CAGCATGGCC	CCTTCACAGG	CATCGCATGC	GGAAAGTCCA	TGATGAGCTC	CGTGAGCCTG	4440
ATGGGGGGCC	GGGGCGGGGT	GCCCCGTGAC	GACCGGAACC	ACGTCACAGG	GGCCTCGTCC	4500
AGCAGCTCGT	CCAGCACGAA	GGCCACGCTG	TACCCGCCGA	TCCTGAACCC	GCCGCCCTCC	4560
CCGGCCACGG	ACCCCTCCCT	GTACAACATG	GACATGTTCT	ACTCTTCAAA	CATTCCGGCC	4620
ACTGCGAGAC	CGTACAGGCC	CTACATCATT	CGAGGAATGG	CGCCCCCGAC	GACGCCCTGC	4680
AGCACCGACG	TGTGTGACAG	CGACTACAGC	GCCAGCCGCT	GGAAGGCCAG	CAAGTACTAC	4740
CTGGATTTGA	ACTCGGACTC	AGACCCCTAT	CCACCCCCAC	CCACGCCCCA	CAGCCAGTAC	4800
CTGTGCGCGG	AGGACAGCTG	CCCGCCCTCG	CCCGCCACCG	AGAGGAGCTA	CTTCCATCTC	4860
TTCCCGCCCC	CTCCGTCCCC	CTGCACGGAC	TCATCCTGAC	CTCGGCCGGG	CCACTCTGGC	4920
TTCTCTGTGC	CCCTGTAAAT	AGTTTTAAAT	ATGAACAAAG	AAAAAAATAT	ATTTTATGAT	4980
TTAAAAATA	AATATAATTG	GGATTTTAAA	AACATGAGAA	ATGTGAAC TG	TGATGGGGTG	5040
GGCAGGGCTG	GGAGAACTTT	GTA 5063	(SEQ ID NO:1)			

## REPLACEMENT FIGURE

**Figure 3**

MEAAPPGPPWPLLLLLLLLLLALCGCPAPAAASPLLLFANRRDVRLVDAGGVKLESTIVVS  
GLEDAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTGAAVQNVVISGLVSPDGLACDWVGK  
KLYWTDSETNRIEVANLNGTSRKVLFWQDLDPRAIALDPAHGYMYWTDWGETPRIERAG  
MDGSTRKIIIVDSDIYWPNGLTIDLEEQKLYWADAKLSFIHRANLDGSFRQKVVEGSLTHP  
FALTLSGDTLYWTDWQTRSIHACNKRTGGKRKEILSALYSPMDIQVLSQERQPPFFHTRCE  
EDNGGCShLCLLSPSEPFYTCACPTGVQLQDNNGRTCKAGAEVLLLARRTDLRRISLDTP  
DFTDIVLQVDDIRHAI AIDYDPLEGYVYWTDDEVRAIRRAYLDGSGAQTLVNTEINDPDG  
IAVDWVARNLYWTDGTDRIEVTRLNGTSRKILVSEDLDPEPRAIALHPVMGLMYWTDWGE  
NPKIECANLDGQERRVLVNASLGWPNGLALDLQEGKLYWGDAKTDKIEVINVDGTKRRTL  
LEDKLPHIFGFTLLGDFIYWTDWQRRS IERVHKVKASRDVIIDQLPDLMLGKAVNNAKV  
GTNPCADRNGGCShLCFFTPHATRCGCPIGLELLSDMKTCIVPEAFLVFTSRAAIHRISL  
ETNNNDVAIPLTGVEASALDFDVSNNH IYWTDVSLKTI SRAFMNGSSVEHVVEFGLDYP  
EGMAVDWMGKNLYWADTGTNR IEVARLDGQFRQVLVWRDLNPRSLALDPTKGYIYWTEW  
GGKPRI VRAFMGTNCMTLVDKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLGQERVV  
IADDLPHPFGLTQYSDI IYWTDWNLHSIERADKTSGRNRTLIQGHLD FVMDILVFHSSRQ  
DGLNDCMHNNGQCGQLCLAI PGGHRCGCASHYTLDPSSRNCSPPTTFLLFSQKSAISRM  
PDDQHSPDLILPLHGLRNVKAIDYDPLDKFIYWVDGRQNIKRAKDDGTQPFVLTSLSQGQ  
NPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLSGEAMGVVLRGDRDKPRAIVVNAERGY  
LYFTNMQDRAAKIERAALDGTEREVLFTTGLIRPVALVVDNTLGKLFWVDADLKRIESC  
LSGANRLTLEDANIVQPLGLTILGKHLWIDRQQQMIERVEKTTGDKRTRIQGRVAHLTG  
IHAVEEVSLEEFSAHPCARDNGGCShICIAKGDGTPRCSCPVHLVLLQNLLTCGEPPTCS  
PDQFACATGEIDCIPGAWRCDGFPECDDQSDEEGCPVCSAAQFPCARGQCVDLRLRCDGE  
ADCQDRSDEADCAICLPNQFRCASGQCVLIKQQCDSFPDCIDGSDELMCEITKPPSDDS  
PAHSSAIGPVIGIILSLFVMGGVYFVCQRVVCQRYAGANGPFPHEYVSGTPHVPLNFIAP  
GGSQHGPFTGIACGKSMMSSVSLMGGRGVPLYDRNHVTGASSSSSSSSTKATLYPPIILNP  
PPSPATDPSLYNMDMFYSSNI PATARPYRPIYIRGMAPPTTPCSTDVCDSDYSASRWKAS  
KYYLDLNSDSDPYPPPPTPHSQYLSAEDSCPPSPATERSYFHLFPPPPSPCTDSS  
(SEQ ID NO:2)

# REPLACEMENT FIGURE

**Figure 5**

NAME	SEQUENCE	SEQ ID NO	LOCATION	PRODUCT SIZE
LRGEN1F	5'-TTG CTG CCC TAG ACT TAG CC-3'	SEQ ID NO:3	-119	406
LRGEN1R	5'-CCA AGT CGC TTC CGA GAC-3'	SEQ ID NO:4	+106	
LRGEN2F	5'-CAT CCC AGG GCT GTG TAT CT-3'	SEQ ID NO:5	-65	543
LRGEN2R	5'-ACT TGG GCT CAT GCA AAT TC-3'	SEQ ID NO:6	+81	
LRGEN3F1	5'-CCG ATG GGT GAG ATT TTA GG-3'	SEQ ID NO:7	-118	329
LRGEN3R1	5'-CGT GGG TAC CTA CCG GAA C-3'	SEQ ID NO:8	+16	
LRGEN4NF	5'-TAA TTG GGT CAG CAG CAA TG-3'	SEQ ID NO:9	-72	277
LRGEN4NR	5'-GCA CTC ACA GAA AGG CTG-3'	SEQ ID NO:10	+8	
LRGEN5NF	5'-AGT GAC GGT CCT CTT CTG GA-3'	SEQ ID NO:11	-51	302
LRGEN5NR	5'-CAA GTG GAT CAT TTC GAA CG-3'	SEQ ID NO:12	+120	
LRGEN6F	5'-TGG CTG AGT ATT TCC CTT GC-3'	SEQ ID NO:13	-95	577
LRGEN6R	5'-CCA GAA TGA CAG GTC CAG GT-3'	SEQ ID NO:14	+85	
LRGEN7F1	5'-TGC TTC TTC TCC AGC CTC AT-3'	SEQ ID NO:15	-14	302
LRGEN7R1	5'-ATG TGG CCA AAT AGC AGA GC-3'	SEQ ID NO:16	+116	
LRGEN8F	5'-GCA TTG AAC CCG TCT TGT TT-3'	SEQ ID NO:17	-109	426
LRGEN8R	5'-GGC ACC TGA GCT CAA CAC TT-3'	SEQ ID NO:18	+100	
LRGEN9F	5'-TGC TGG GCT GTT GTG TTT A-3'	SEQ ID NO:19	-47	407
LRGEN9R	5'-CTT TGA GGC AGG AAC AGA GG-3'	SEQ ID NO:20	+70	
LRGEN10F	5'-AGC GAA ACT CCG TCT CAA AA-3'	SEQ ID NO:21	-79	417
LRGEN10R	5'-GCT CTA ATC ACT GAG GGC CA-3'	SEQ ID NO:22	+110	
LRGEN11F1	5'-GAG GGC TGA GCT GAA GAG GT-3'	SEQ ID NO:23	-105	398
LRGEN11R1	5'-CAG GTT GGG GAA CTT GCA G-3'	SEQ ID NO:24	+108	
LRGEN12F	5'-ATT CAT GTG GTC GCT AGG CT-3'	SEQ ID NO:25	-113	479
LRGEN12R	5'-GAA GCT CCT TTC AGC GTC AG-3'	SEQ ID NO:26	+40	
LRGEN13F	5'-CCA GCT CCT CTG TGG CTT AC-3'	SEQ ID NO:27	-57	352
LRGEN13R	5'-TCC TCC CTC TGC TAA GGA CA-3'	SEQ ID NO:28	+95	
LRGEN14F	5'-CAG AGC TCT CCA GCC AGT G-3'	SEQ ID NO:29	-149	440
LRGEN14R	5'-CTG TGA GAG GCT GGC ATT C-3'	SEQ ID NO:30	+82	
LRGEN15NF	5'-ATG TGA CCT GTC AGC CTC G-3'	SEQ ID NO:31	-131	415
LRGEN15NR	5'-TGC TGC CAT TAC TGA CAA TGA-3'	SEQ ID NO:32	+83	
LRGEN16F	5'-TCT GTC CTC CCA AGC TGA GT-3'	SEQ ID NO:33	-76	374
LRGEN16R	5'-CAC ACA GGA TCT TGC ACT GG-3'	SEQ ID NO:34	+88	
LRGEN17F	5'-CAT GAG TTC TCA TTT GGC CC-3'	SEQ ID NO:35	-92	321
LRGEN17R	5'-GCC ACA GGG ACT GTG ATT TT-3'	SEQ ID NO:36	+103	
LRGEN18F	5'-CAA CTT CTG CTT TGA AGC CC-3'	SEQ ID NO:37	-88	423
LRGEN18R	5'-CAG AGC CCC TAC TCC TGT GA-3'	SEQ ID NO:38	+98	
LRGEN19F	5'-CCA GAC CTT GGT TGC TGT G-3'	SEQ ID NO:39	-81	269
LRGEN19R	5'-CGT CTC CTC CCC TAA ACT CC-3'	SEQ ID NO:40	+77	
LRGEN20NF	5'-ATG TTG GCC ACC TCT TTC TG-3'	SEQ ID NO:41	-34	310
LRGEN20NR	5'-CTG CCT CCT CCA GAT CAT TC-3'	SEQ ID NO:42	+39	
LRGEN21F	5'-GAG TCT CGT GGG TAG TGG GA-3'	SEQ ID NO:43	-102	373
LRGEN21R	5'-AGA AAG CAA GCA TGC CTC AG-3'	SEQ ID NO:44	+131	
LRGEN22F	5'-AGC CCT CTC TGC AAG GAA AG-3'	SEQ ID NO:45	-96	305
LRGEN22R	5'-GCC CAC TAG CAC CCA GAA TA-3'	SEQ ID NO:46	+111	
LRGEN23F	5'-GAC AGG CCT TTC CCG TTC-3'	SEQ ID NO:47	-95	650
LRGEN23R	5'-CAG GAG GAC TCT CAT GGT GG-3'	SEQ ID NO:48	+106	
LRCOD1F	5'-TTC GTC ATG GGT GGT GTC TA-3'	SEQ ID NO:49	4192	416

# REPLACEMENT FIGURE

**Figure 5**

LRCOD1R	5'-TTC CTC GAA TGA TGT AGG GC-3'	SEQ ID NO:50	4607	
LRCOD2F	5'-ACC TGG ACT TCG TGA TGG AC-3'	SEQ ID NO:51	2654	466
LRCOD2R	5'-CAG AAC AGT GTC CGG CTG TA-3'	SEQ ID NO:52	3119	
LRCOD3F	5'-CCA TGG AGC CCG AGT GAG-3'	SEQ ID NO:53	-50	504
LRCOD3R	5'-GTC AAG GTC CTG CCA GAA GA-3'	SEQ ID NO:54	453	
LRCOD4F	5'-GGG CAA GAA GCT GTA CTG GA-3'	SEQ ID NO:55	354	500
LRCOD4R	5'-TGG ATG TCC ATG GGT GAG TA-3'	SEQ ID NO:56	853	
LRCOD5F	5'-CAG ACC CGC TCC ATC CAT-3'	SEQ ID NO:57	767	484
LRCOD5R	5'-TCG TTG ATC TCG GTG TTG AC-3'	SEQ ID NO:58	1250	
LRCOD6F	5'-ATC GAC TAC GAC CCG CTA GA-3'	SEQ ID NO:59	1132	546
LRCOD6R	5'-GTA GAT GAA GTC CCC CAG CA-3'	SEQ ID NO:60	1677	
LRCOD7F	5'-GCC AAG ACA GAC AAG ATC GAG-3'	SEQ ID NO:61	1564	505
LRCOD7R	5'-TGT GGT TGT TGG ACA CAT CA-3'	SEQ ID NO:62	2068	
LRCOD8F	5'-CAC AGG ATC TCC CTC GAG AC-3'	SEQ ID NO:63	1966	522
LRCOD8R	5'-CTC GAT CAT GTT GGT GTC CA-3'	SEQ ID NO:64	2487	
LRCOD9F	5'-CAG CCC TTT GTT TTG ACC TC-3'	SEQ ID NO:65	3025	484
LRCOD9R	5'-TCC AGT AGA GAT GCT TGC CA-3'	SEQ ID NO:66	3508	
LRCOD10F	5'-AAG CGC ATT GAG AGC TGT G-3'	SEQ ID NO:67	3400	480
LRCOD10R	5'-CTC CTC GTC GCT CTG GTC-3'	SEQ ID NO:68	3879	
LRCOD11F	5'-CAC AGG GGA GAT CGA CTG TAT-3'	SEQ ID NO:69	3801	480
LRCOD11R	5'-ACA TAC TCG TGC GGG AAG G-3'	SEQ ID NO:70	4280	
LRCOD12F	5'-GTC CAG CAG CTC GTC CAG-3'	SEQ ID NO:71	4446	567
LRCOD12R	5'-TAC AAA GTT CTC CCA GCC CT-3'	SEQ ID NO:72	5012	
LRCOD13F	5'-TCA TGG ACG GGA CCA ACT-3'	SEQ ID NO:73	2369	431
LRCOD13R	5'-GGT GTA GTG TGA GGC GCA G-3'	SEQ ID NO:74	2799	

## REPLACEMENT FIGURE

### Figure 6

#### BSMR Construct Information

The following BSMR expression constructs have been constructed using the pcDNA3 expression vector for use in following BSMR expression, function, and other biological (e.g. ligand and downstream signaling) interactions.

1. A full length wild type construct extending from primers LRCOD3F to LRCOD12R.

Sequence encoding a FLAG<sup>®</sup> antibody epitope 5'-GAC TAC AAG GAC GAC GAT GAC AAG-3' (SEQ ID NO:84) was inserted into the wild-type construct immediately downstream of nucleotide 165 (relative to the "A" in the ATG translation start site). This construct expresses a BSMR protein which has a FLAG<sup>®</sup> epitope between wild type BSMR amino acid residues 55 and 56.

This was accomplished using the following primer sequences and using a site-directed mutagenesis reaction sold under the trademark QUICKCHANGE<sup>®</sup>:

LRPFLAGF: 5'-GAC TAC AAG GAC GAC GAT GAC AAG ACC ATC GTG GTC AGC GGC CTG-3' (SEQ ID NO:85)

LRPFLAGR: 5'-CTT GTC ATC GTC GTC CTT GTA GGA CTC CAG CTT GAC TCC GCC-3' (SEQ ID NO:86)

Sequence encoding a MYC antibody epitope 5'-GAC CAG AAG CTG ATA TCC GAG GAG GAC CTG-3' (SEQ ID NO:87) was inserted immediately upstream of the stop codon after residue 4845 (relative to the "A" in the ATG translation start site). The construct expresses a BSMR protein which has a MYC epitope at the end of the wild type BSMR polypeptide.

This was accomplished using the following primer sequences and using a site-directed mutagenesis reaction sold under the trademark QUICKCHANGE<sup>®</sup>:

LRPMYCF: 5'-GAG CAG AAG CTG ATA TCC GAG GAG GAC CTG TGA CCT CGG CCG GGC-3' (SEQ ID NO:88)

LRPMYCR: 5'-CAG GTC CTC CTC GGA TAT CAG CTT CTG CTC GGA TGA GTC CGT GCA-3' (SEQ ID NO:89)

An expression construct containing both the FLAG<sup>®</sup> and MYC antibody epitopes at the aforementioned sites has also been produced.

## REPLACEMENT FIGURE

### Figure 13

RVRLASHLRKLRK (SEQ ID NO:75)

RLTRKRGLKLA (SEQ ID NO:76)

CRAKRNNFKSA (SEQ ID NO:77)

LKWKS (SEQ ID NO:78)

KIRVKAGETQKKVIFCSREKVSHL (SEQ ID NO:79)

FIPLKPTVKMLERSNHVSRTEVSSNHV (SEQ ID NO:80)

DKGMAPALRHLYKELMGPWN (SEQ ID NO:81)

DALKLAIDNALSIT (SEQ ID NO:82)